

SEQUENCE LISTING

<110> Max-Planck-Gesellschaft zur Förderung der Wissensc

<120> L-amino acid oxidase with cytotoxic activity from
Aplysia punctata

<130> 29644PWO_2

<140> PCT/EP04/00423

<141> 2004-01-20

<150> EP03001232.2

<151> 2003-01-20

<150> EP03026613.4

<151> 2003-11-19

<160> 72

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Aplysia punctata

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 Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala
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 Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe
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 gag tac tca gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg ccc 240
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 Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe
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tca	ctg	aaa	gat	gag	gtc	tac	gtg	gtg	gga	gcc	gat	tac	tcc	tgg	gga	1536				
Ser	Leu	Lys	Asp	Glu	Val	Tyr	Val	Val	Gly	Ala	Asp	Tyr	Ser	Trp	Gly					
			500				505						510							
ctt	atc	tcc	tcc	tgg	ata	gag	ggc	gct	ctg	gag	acc	tca	gaa	aac	gtc	1584				
Leu	Ile	Ser	Ser	Trp	Ile	Glu	Gly	Ala	Leu	Glu	Thr	Ser	Glu	Asn	Val					
			515				520						525							
atc	aac	gac	tac	ttc	ctc	taa										1605				
Ile	Asn	Asp	Tyr	Phe	Leu															
			530				535													

<210> 4

<211> 534

<212> PRT

<213> *Aplysia punctata*

<400> 4

Ser	Ser	Ala	Val	Leu	Leu	Leu	Ala	Cys	Ala	Leu	Val	Ile	Ser	Val	His
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Ala	Asp	Gly	Val	Cys	Arg	Asn	Arg	Arg	Gln	Cys	Asn	Arg	Glu	Val	Cys
			20					25					30		

Gly	Ser	Thr	Tyr	Asp	Val	Ala	Val	Val	Gly	Ala	Gly	Pro	Gly	Gly	Ala
		35					40					45			

Asn	Ser	Ala	Tyr	Met	Leu	Arg	Asp	Ser	Gly	Leu	Asp	Ile	Ala	Val	Phe
	50					55					60				

Glu	Tyr	Ser	Asp	Arg	Val	Gly	Gly	Arg	Leu	Phe	Thr	Tyr	Gln	Leu	Pro
65					70					75					80

Asn	Thr	Pro	Asp	Val	Asn	Leu	Glu	Ile	Gly	Gly	Met	Arg	Phe	Ile	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				85				90				95			
Gly	Ala	Met	His	Arg	Leu	Trp	Arg	Val	Ile	Ser	Glu	Leu	Gly	Leu	Thr
			100										110		
Pro	Lys	Val	Phe	Lys	Glu	Gly	Phe	Gly	Lys	Glu	Gly	Arg	Gln	Arg	Phe
			115										125		
Tyr	Leu	Arg	Gly	Gln	Ser	Leu	Thr	Lys	Lys	Gln	Val	Lys	Ser	Gly	Asp
			130										140		
Val	Pro	Tyr	Asp	Leu	Ser	Pro	Glu	Glu	Lys	Glu	Asn	Gln	Gly	Asn	Leu
Val	Glu	Tyr	Tyr	Leu	Glu	Lys	Leu	Thr	Gly	Leu	Gln	Leu	Asn	Gly	Glu
Pro	Leu	Lys	Arg	Glu	Val	Ala	Leu	Lys	Leu	Thr	Val	Pro	Asp	Gly	Arg
			180										190		
Phe	Leu	Tyr	Asp	Leu	Ser	Phe	Asp	Glu	Ala	Met	Asp	Leu	Val	Ala	Ser
			195										205		
Pro	Glu	Gly	Lys	Glu	Phe	Thr	Arg	Asp	Thr	His	Val	Phe	Thr	Gly	Glu
			210										220		
Val	Thr	Leu	Gly	Ala	Ser	Ala	Val	Ser	Leu	Phe	Asp	Asp	His	Leu	Gly
			225												
Glu	Asp	Tyr	Tyr	Gly	Ser	Glu	Ile	Tyr	Thr	Leu	Lys	Glu	Gly	Leu	Ser
			245										255		
Ser	Val	Pro	Gln	Gly	Leu	Leu	Gln	Ala	Phe	Leu	Asp	Ala	Ala	Asp	Ser
			260										270		
Asn	Glu	Phe	Tyr	Pro	Asn	Ser	His	Leu	Lys	Ala	Leu	Arg	Arg	Lys	Thr
			275										285		
Asn	Gly	Gln	Tyr	Val	Leu	Tyr	Phe	Glu	Pro	Thr	Thr	Ser	Lys	Asp	Gly
			290										300		
Gln	Thr	Thr	Ile	Asn	Tyr	Leu	Glu	Pro	Leu	Gln	Val	Val	Cys	Ala	Gln
			305										315		
Arg	Val	Ile	Leu	Ala	Met	Pro	Val	Tyr	Ala	Leu	Asn	Gln	Leu	Asp	Trp
			325										335		
Asn	Gln	Leu	Arg	Asn	Asp	Arg	Ala	Thr	Gln	Ala	Tyr	Ala	Ala	Val	Arg
			340										350		
Pro	Ile	Pro	Ala	Ser	Lys	Val	Phe	Met	Thr	Phe	Asp	Gln	Pro	Trp	Trp
			355										365		
Leu	Glu	Asn	Glu	Arg	Lys	Ser	Trp	Val	Thr	Lys	Ser	Asp	Ala	Leu	Phe
			370										380		

Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile
 385 390 395 400
 Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu
 405 410 415
 Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn
 420 425 430
 Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu
 435 440 445
 Ala Tyr Gly Val Glu Arg Asp Ser Ile Arg Glu Pro Val Thr Ala Ala
 450 455 460
 Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp
 465 470 475 480
 Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro
 485 490 495
 Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly
 500 505 510
 Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val
 515 520 525
 Ile Asn Asp Tyr Phe Leu
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<210> 5
 <211> 1554
 <212> DNA
 <213> *Aplysia punctata*

<220>
 <221> CDS
 <222> (1)..(1554)

<400> 5
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 1 5 10 15
 tct acc tac gat gtg gct gtc gtg ggg gcg ggg cct ggg gga gct aac 96
 Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn
 20 25 30
 tcc gcc tac atg ctg agg gac tcc gcc ctg gac atc gct gtg ttc gag 144
 Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
 35 40 45
 tac tca gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg ccc aac 192
 Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn
 50 55 60

aca ccc gac gtt aat ctc gag att ggc ggc atg agg ttc atc gag ggc	240
Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu Gly	
65 70 75 80	
gcc atg cac agg ctc tgg agg gtc att tca gaa ctc ggc cta acc ccc	288
Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr Pro	
85 90 95	
aag gtg ttc aag gaa ggt ttc gga aag gag ggc aga cag aga ttt tac	336
Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe Tyr	
100 105 110	
ctg cgg gga cag agc ctg acc aag aaa cag gtc aag agt ggg gac gta	384
Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp Val	
115 120 125	
ccc tat gac ctc agc ccg gag gag aaa gaa aac cag gga aat ctg gtc	432
Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu Val	
130 135 140	
gaa tac tac ctg gag aaa ctg aca ggt cta aaa ctc aac ggc gga ccg	480
Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Lys Leu Asn Gly Gly Pro	
145 150 155 160	
ctc aaa cgt gag gtt gcg ctt aaa cta acc gtg ccg gac ggc aga ttc	528
Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg Phe	
165 170 175	
ctc tat gac ctc tcg ttt gac gaa gcc atg gac ctg gtt gcc tcc cct	576
Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser Pro	
180 185 190	
gag ggc aaa gag ttc acc cga gac acg cac gtg ttc acc gga gaa gtc	624
Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu Val	
195 200 205	
acc ctg gac gcg tcg gct gtc tcc ctc ttc gac gac cac ctg gga gag	672
Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly Glu	
210 215 220	
gac tac tat ggc agt gag atc tac acc cta aag gaa gga ctg tct tcc	720
Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser Ser	
225 230 235 240	
gtc cca caa ggg ctc cta cag act ttt ctg gac gcc gca gac tcc aac	768
Val Pro Gln Gly Leu Leu Gln Thr Phe Leu Asp Ala Ala Asp Ser Asn	
245 250 255	
gag ttc tat ccc aac agc cac ctg aag gcc ctg aga cgt aag acc aac	816
Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr Asn	
260 265 270	
ggt cag tat gtt ctt tac ttt gag ccc acc acc tcc aag gat gga caa	864
Gly Gln Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln	
275 280 285	

acc aca atc aac tat ctg gaa ccc ctg cag gtt gtg tgt gca cag aga	912
Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg	
290 295 300	
gtc atc ctg gcc atg ccg gtc tac gct ctc aac caa ctg gac tgg aat	960
Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn	
305 310 315 320	
cag ctc aga aat gac cga gcc acc caa gcg tac gct gcc gtg cgc ccg	1008
Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Val Arg Pro	
325 330 335	
att cct gca agt aaa gtg ttc atg acc ttt gat cag ccc tgg tgg ttg	1056
Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu	
340 345 350	
gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt ttc agc	1104
Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser	
355 360 365	
caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac atc ctg	1152
Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu	
370 375 380	
atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg gag ctg	1200
Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu Leu	
385 390 395 400	
aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac aac cag	1248
Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln	
405 410 415	
gtc acc gaa ccc ctc aag gac acc att ctt gac cac ctc act gag gct	1296
Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala	
420 425 430	
tat ggc gtg gaa cga gac tcg atc ccg gaa ccc gtg acc gcc gct tcc	1344
Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser	
435 440 445	
cag ttc tgg acc gac tac ccg ttc ggc tgt gga tgg atc acc tgg agg	1392
Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg	
450 455 460	
gca ggc ttc cat ttt gat gac gtc atc agc acc atg cgt cgc ccg tca	1440
Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser	
465 470 475 480	
ctg aaa gat gag gtc tac gtg gtg gga gcc gat tac tcc tgg gga ctt	1488
Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu	
485 490 495	
atc tcc tcc tgg ata gag ggc gct ctg gag acc tcg gaa aac gtc atc	1536
Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile	
500 505 510	
aac gac tac ttc ctc taa	1554

Asn Asp Tyr Phe Leu
515

<210> 6
<211> 517
<212> PRT
<213> *Aplysia punctata*

<400> 6
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Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn
20 25 30
Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
35 40 45
Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn
50 55 60
Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu Gly
65 70 75 80
Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr Pro
85 90 95
Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe Tyr
100 105 110
Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp Val
115 120 125
Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu Val
130 135 140
Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Lys Leu Asn Gly Gly Pro
145 150 155 160
Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg Phe
165 170 175
Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser Pro
180 185 190
Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu Val
195 200 205
Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly Glu
210 215 220
Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser Ser
225 230 235 240
Val Pro Gln Gly Leu Leu Gln Thr Phe Leu Asp Ala Ala Asp Ser Asn
245 250 255

Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr Asn
 260 265 270
 Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln
 275 280 285
 Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg
 290 295 300
 Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn
 305 310 315 320
 Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro
 325 330 335
 Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu
 340 345 350
 Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser
 355 360 365
 Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu
 370 375 380
 Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu Leu
 385 390 395 400
 Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln
 405 410 415
 Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala
 420 425 430
 Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser
 435 440 445
 Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg
 450 455 460
 Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser
 465 470 475 480
 Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu
 485 490 495
 Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile
 500 505 510
 Asn Asp Tyr Phe Leu
 515

<210> 7

<211> 600

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)..(600)

<400> 7

atg tct tca gga aat gct aaa att ggg cac cct gcc ccc aac ttc aaa	48
Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys	
1 5 10 15	
gcc aca gct gtt atg cca gat ggt cag ttt aaa gat atc agc ctg tct	96
Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser	
20 25 30	
gac tac aaa gga aaa tat gtt gtg ttc ttc ttt tac cct ctt gac ttc	144
Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe	
35 40 45	
acc ttt gtg tgc ccc acg gag atc att gct ttc agt gat agg gca gaa	192
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu	
50 55 60	
gaa ttt aag aaa ctc aac tgc caa gtg att ggt gct tct gtg gat tct	240
Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser	
65 70 75 80	
cac ttc tgt cat cta gca tgg gtc aat aca cct aag aaa caa gga gga	288
His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly	
85 90 95	
ctg gga ccc atg aac att cct ttg gta tca gac ccg aag cgc acc att	336
Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile	
100 105 110	
gct cag gat tat ggg gtc tta aag gct gat gaa ggc atc tcg ttc agg	384
Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg	
115 120 125	
ggc ctt ttt atc att gat gat aag ggt att ctt cgg cag atc act gta	432
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val	
130 135 140	
aat gac ctc cct gtt ggc cgc tct gtg gat gag act ttg aga cta gtt	480
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val	
145 150 155 160	
cag gcc ttc cag ttc act gac aaa cat ggg gaa gtg tgc cca gct ggc	528
Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly	
165 170 175	
tgg aaa cct ggc agt gat acc atc aag cct gat gtc caa aag agc aaa	576
Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys	
180 185 190	
gaa tat ttc tcc aag cag aag tga	600
Glu Tyr Phe Ser Lys Gln Lys	

195

200

<210> 8
 <211> 199
 <212> PRT
 <213> Human

<400> 8
 Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys
 1 5 10 15
 Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser
 20 25 30
 Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe
 35 40 45
 Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
 50 55 60
 Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
 65 70 75 80
 His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly
 85 90 95
 Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
 100 105 110
 Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
 115 120 125
 Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
 130 135 140
 Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
 145 150 155 160
 Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
 165 170 175
 Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys
 180 185 190
 Glu Tyr Phe Ser Lys Gln Lys
 195

<210> 9
 <211> 19
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic

double-stranded RNA molecule

<400> 9
ggcugaugaa ggcaucucg 19

<210> 10
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 10
augcuaaaau ugggcaccc 19

<210> 11
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 11
ugcuaaaau qggcacccu 19

<210> 12
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 12
cuucaaagcc acagcuguu 19

<210> 13
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 13
agccacagcu guuaugcca 19

<210> 14
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 14
gccacagcug uuaugccag 19

<210> 15
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 15
agauaucagc cugucugac 19

<210> 16
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 16
gauaucagcc ugucugacu 19

<210> 17
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 17
gaaacucaac ugccaagug 19

<210> 18
<211> 19
<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 18

acucaacugc caagugauu

19

<210> 19

<211> 19

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 19

cucaacugcc aagugauug

19

<210> 20

<211> 19

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 20

cugccaagug auuggugcu

19

<210> 21

<211> 19

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 21

gugauuggug cuucugugg

19

<210> 22

<211> 19

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 22
gaaacaagga ggacuggga 19

<210> 23
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 23
cauuccuuug guaucagac 19

<210> 24
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 24
aggcugauga aggcaucuc 19

<210> 25
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 25
gcgcaccāuu gcucaggau 19

<210> 26
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 26
ggguauucuu cggcagauc 19

<210> 27
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 27
accuggcagu gauaccauc 19

<210> 28
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 28
ccuggcagug auaccauca 19

<210> 29
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 29
gccugauguc caaaagagc 19

<210> 30
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 30
cuggacuucc agaagaaca 19

<210> 31
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 31
cuuacgcuga guacuucga

19

<210> 32
<211> 7
<212> PRT
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<400> 32
Asp Gly Glu Asp Ala Ala Val
1 5

<210> 33
<211> 9
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (1)
<223> Asp can be Asp or Gln

<220>
<221> MOD_RES
<222> (3)
<223> Ile can be Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Gln can be Gln or Arg

<220>
<221> MOD_RES
<222> (9)
<223> Pro can be Pro or Gln

<400> 33
Asp Gly Ile Cys Arg Asn Gln Arg Pro
1 5

<210> 34
<211> 4
<212> PRT
<213> Aplysia

<400> 34

Phe Ala Asp Ser

1

<210> 35

<211> 8

<212> PRT

<213> Aplysia

<220>

<221> MOD_RES

<222> (5)

<223> Ile can be Ile or Leu

<400> 35

Gly Pro Asp Gly Ile Val Ala Asp

1

5

<210> 36

<211> 7

<212> PRT

<213> Aplysia

<220>

<221> MOD_RES

<222> (6)

<223> Lys can be Lys or Gln

<220>

<221> MOD_RES

<222> (7)

<223> Ile can be Ile or Leu

<400> 36

Pro Gly Glu Val Ser Lys Ile

1

5

<210> 37

<211> 15

<212> PRT

<213> Aplysia

<400> 37

Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro Ile Pro Ala Ser Lys

1

5

10

15

<210> 38

<211> 13

<212> PRT

<213> Aplysia

<400> 38

Asp Ser Gly Leu Asp Ile Ala Val Glu Tyr Ser Asp Arg
1 5 10

<210> 39

<211> 12

<212> PRT

<213> Aplysia

<400> 39

Gly Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys
1 5 10

<210> 40

<211> 442

<212> DNA

<213> Aplysia

<400> 40

caagacgggg aagacaagga gtttgacgga gaaatcgta gcgtcagagt gctgaaggcg 60
ttcggcaagc ctggctacgg ttacaagcag ccctcgtgca aggaaggcaa ggactacgtg 120
agcagcggca gcgttcttca cgtgctgcag tgtgccggct tcttcgaggt gtgctacgag 180
gagaggatca ccacccagcc agccacgact gtcgctgcag cagaggatca atgcaaaaag 240
ttcatcgcaa cccacaaatt ggaggagact gttgatggaa ggatcgtcag catcgagctt 300
gtccagagac tgaagaaaca atccggatac ggtccaagtg gcggttctgg ttatggcaac 360
ggtcatggtc aaagacccgg ttacggatac ggttctggta gtggaagtgg ctacgcccc 420
agaggaggat acaacccaaa ag 442

<210> 41

<211> 147

<212> PRT

<213> Aplysia

<400> 41

Gln Asp Gly Glu Asp Lys Glu Phe Asp Gly Glu Ile Val Ser Val Arg
1 5 10 15

Val Leu Lys Ala Phe Gly Lys Pro Gly Tyr Gly Tyr Lys Gln Pro Ser
20 25 30

Cys Lys Glu Gly Lys Asp Tyr Val Ser Ser Gly Ser Val Leu His Val
35 40 45

Leu Gln Cys Ala Gly Phe Phe Glu Val Cys Tyr Glu Glu Arg Ile Thr
50 55 60

Thr Gln Pro Ala Thr Thr Val Ala Ala Ala Glu Val Gln Cys Lys Lys
65 70 75 80

Phe Ile Ala Thr His Lys Leu Glu Glu Thr Val Asp Gly Arg Ile Val
85 90 95

Ser Ile Glu Leu Val Gln Arg Leu Lys Lys Gln Ser Gly Tyr Gly Pro
100 105 110

Ser Gly Gly Ser Gly Tyr Gly Asn Gly His Gly Gln Arg Pro Gly Tyr
115 120 125

Gly Tyr Gly Ser Gly Ser Gly Ser Gly Tyr Ala Pro Arg Gly Gly Tyr
130 135 140

Asn Pro Lys
145

<210> 42
<211> 462
<212> DNA
<213> Aplysia

<400> 42
taccgcccc gccaccactn tngcaccagc agaaccaacc tgcgagaagc tgtccgntg 60
gttcaacgtg ganaagaaat tcgaagggtc cagaatcgtg agtttcaagc tcatccgcct 120
gttcaacagg tncaagaagt gcaagaaagn ccagtattcc gtgtctggcg atgatgagga 180
cncattcggt gtcagtgggt gttctggcgt gttccaggtg tgctacgaag aacaaacggc 240
gcccgtaca accnccacag aagccccgaa gccagagcca agaagacca agaggaaaaa 300
tttcccaatc aaatttngta aacactgatg gggttaatntg acgaccagtg cgtctgcgaa 360
agaatcatgt tatggttcat gatgtcatgc tcttaatat ggttgtaacg tttaacgcga 420
tacagacatt aaaactcatt gttcaaaaaa aaaaaaaaaa aa 462

<210> 43
<211> 155
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (1)..(155)
<223> Xaa = unknown amino acid or STOP-codon

<400> 43
Tyr Arg Pro Arg His His Xaa Xaa Thr Ser Arg Thr Asn Leu Arg Glu
1 5 10 15

Ala Val Arg Xaa Val Gln Arg Gly Xaa Glu Ile Arg Arg Phe Gln Asn
20 25 30

Arg Glu Phe Gln Ala His Pro Pro Val Gln Gln Xaa Gln Glu Val Gln
35 40 45

Glu Xaa Pro Val Phe Arg Val Trp Arg Xaa Xaa Gly Xaa Ile Arg Cys
50 55 60

Gln Trp Leu Phe Trp Arg Val Pro Gly Xaa Leu Arg Arg Thr Asn Gly
65 70 75 80

Ala Arg Tyr Asn Xaa His Arg Ser Pro Glu Ala Arg Ala Lys Lys Thr
85 90 95
Gln Glu Glu Lys Phe Pro Asn Gln Ile Xaa Xaa Thr Leu Met Gly Xaa
100 105 110
Xaa Asp Asp Gln Cys Val Cys Glu Arg Ile Met Leu Trp Phe Met Met
115 120 125
Ser Cys Ser Xaa Xaa Tyr Arg Leu Xaa Arg Leu Thr Arg Tyr Arg His
130 135 140
Xaa Asn Ser Leu Phe Lys Lys Lys Lys Lys Lys
145 150 155

<210> 44
<211> 153
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (1)..(153)
<223> Xaa = unknown amino acid or STOP-codon

<400> 44
Thr Ala Pro Ala Thr Thr Xaa Ala Pro Ala Glu Pro Thr Cys Glu Lys
1 5 10 15
Leu Ser Xaa Trp Phe Asn Val Xaa Lys Lys Phe Glu Gly Ser Arg Ile
20 25 30
Val Ser Phe Lys Leu Ile Arg Leu Phe Asn Arg Xaa Lys Lys Cys Lys
35 40 45
Lys Xaa Gln Tyr Ser Val Ser Gly Asp Asp Glu Asp Xaa Phe Val Val
50 55 60
Ser Gly Cys Ser Gly Val Phe Gln Xaa Cys Tyr Glu Glu Gln Thr Ala
65 70 75 80
Pro Ala Thr Thr Xaa Thr Glu Ala Pro Lys Pro Glu Pro Arg Arg Pro
85 90 95
Lys Arg Lys Asn Phe Pro Ile Lys Phe Xaa Lys His Xaa Trp Val Asn
100 105 110
Xaa Thr Thr Ser Ala Ser Ala Lys Glu Ser Cys Tyr Gly Ser Xaa Cys
115 120 125
His Ala Leu Asn Ile Gly Cys Asn Val Xaa Arg Asp Thr Asp Ile Lys
130 135 140
Thr His Cys Ser Lys Lys Lys Lys Lys
145 150

<210> 45
<211> 153
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (1)..(153)
<223> Xaa = unknown amino acid or STOP-codon

<400> 45
Pro Pro Pro Pro Pro Xaa Xaa His Gln Gln Asn Gln Pro Ala Arg Ser
1 5 10 15
Cys Pro Xaa Gly Ser Thr Trp Xaa Arg Asn Ser Lys Val Pro Glu Ser
20 25 30
Xaa Val Ser Ser Ser Ser Ala Cys Ser Thr Gly Xaa Arg Ser Ala Arg
35 40 45
Lys Xaa Ser Ile Pro Cys Leu Ala Met Met Arg Xaa His Ser Leu Ser
50 55 60
Val Val Val Leu Ala Cys Ser Arg Xaa Ala Thr Lys Asn Lys Arg Arg
65 70 75 80
Pro Leu Gln Xaa Pro Gln Lys Pro Arg Ser Gln Ser Gln Glu Asp Pro
85 90 95
Arg Gly Lys Ile Ser Gln Ser Asn Xaa Val Asn Thr Asp Gly Leu Xaa
100 105 110
Xaa Arg Pro Val Arg Leu Arg Lys Asn His Val Met Val His Asp Val
115 120 125
Met Leu Leu Ile Xaa Val Val Thr Phe Asn Ala Ile Gln Thr Leu Lys
130 135 140
Leu Ile Val Gln Lys Lys Lys Lys Lys
145 150

<210> 46
<211> 9
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (3)
<223> Ile can be Ile or Val

<400> 46

Asp Gly Ile Cys Arg Asn Arg Arg Gln
1 5

<210> 47
<211> 14
<212> PRT
<213> Aplysia

<400> 47
Asp Ser Gly Leu Asp Ile Ala Val Phe Glu Tyr Ser Asp Arg
1 5 10

<210> 48
<211> 7
<212> PRT
<213> Aplysia

<400> 48
Val Phe Glu Tyr Ser Asp Arg
1 5

<210> 49
<211> 16
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = any amino acid, in particular Thr

<400> 49
Leu Phe Xaa Tyr Gln Leu Pro Asn Thr Pro Asp Val Asn Leu Glu Ile
1 5 10 15

<210> 50
<211> 10
<212> PRT
<213> Aplysia

<400> 50
Val Ile Ser Glu Leu Gly Leu Thr Pro Lys
1 5 10

<210> 51
<211> 11

<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = any amino acid, in particular Met

<400> 51
Val Ile Leu Ala Xaa Pro Val Tyr Ala Leu Asn
1 5 10

<210> 52
<211> 8
<212> PRT
<213> Aplysia

<400> 52
Val Phe Met Thr Phe Asp Gln Pro
1 5

<210> 53
<211> 10
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (6)
<223> Phe can be Phe or Ser

<400> 53
Ser Asp Ala Leu Phe Phe Gln Met Tyr Asp
1 5 10

<210> 54
<211> 18
<212> PRT
<213> Aplysia

<400> 54
Ser Glu Ala Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly
1 5 10 15

Leu Lys

<210> 55

<211> 21
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (12)
<223> Gln can be Gln or Gly

<400> 55
Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gln Tyr Asn Gln Val
1 5 10 15
Thr Glu Pro Leu Lys
20

<210> 56
<211> 28
<212> PRT
<213> Aplysia

<400> 56
Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn Ser Ala Tyr Met
1 5 10 15
Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
20 25

<210> 57
<211> 8
<212> PRT
<213> Aplysia

<400> 57
Arg Val Gly Gly Arg Leu Phe Thr
1 5

<210> 58
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
tcctaacgta ggtctagacc tggtgcattt tttttttttt ttttt

45

<210> 59

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<223> n = i

<400> 59
tcgtgttcga rtactcngay cg

22

<210> 60
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 60
ctgtaggtct agacctgttg ca

22

<210> 61
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 61
ccgtgtagat ctcaactgcca ta

22

<210> 62
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 62
ccgttgagtt gtagacct

18

<210> 63
<211> 36
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<223> n = 1

<400> 63

ggccacgcgt cgactagtac gggnnngggnn gggnnng

36

<210> 64

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 64

aattggccac gcgtcgacta gtac

24

<210> 65

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 65

aattctcgtc tgctgtgctt ctctt

25

<210> 66

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 66

gacttagagg aagtagtcgt tga

23

<210> 67

<211> 20

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 67
ctgttatgcc agatggtcag 20

<210> 68
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 68
gtacttgtaa ggaaaccata g 21

<210> 69
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 69
caagaaggag ggtgacctga 20

<210> 70
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 70
ttcgttgaag tcctactcta cg 22

<210> 71
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 71
ggtatcgtgg aaggactcat gac 23

<210> 72
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 72
gacttgccct tcgagtgacc gta